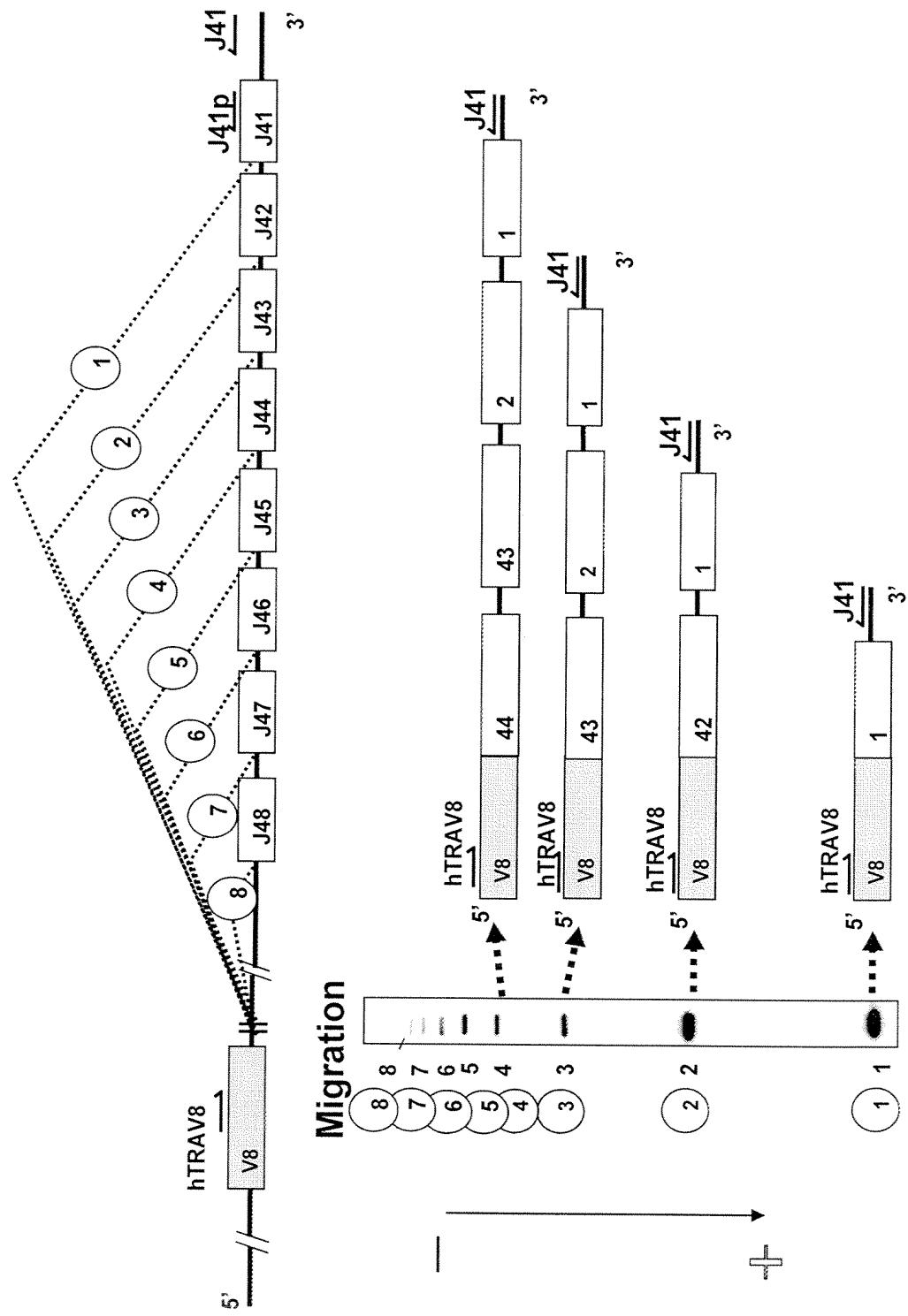


Figure 4



hv gene	Heptamer	SEQ ID NO	%	Spacer	SEQ ID NO	%	Nonamer	SEQ ID NO	%	RSS score	Dist/Ca (Kb)	Signal Qty	J tropism
hV1-1	CACAGTG	76	100	ACTATGAGGCCCTCTTAACCTGTG	77	56	CCAAATTC	78	56	72	925	1604	J10
hV1-2	CACGGTG	79	86	ACTATGAGCCCTCTTACCTGTGCA	80	63	CCAAATTC	78	56	69	904	1604	J10
hV2	CACAGAC	81	86	GCAGGGAAACCCATGAAAGAGCTGA	82	56	ACAGAAACA	83	78	75	835	1637	J10
hV3	CACACTG	84	86	ATAGGCCGCTGCAAGGGGAGCAGA	85	56	ACACAAACT	86	89	80	824	1940	J10
hV5	CACATG	87	86	CTTCTCAGGCACCTGTATCCGT	88	94	ACCCAAACC	89	100	93	798	2406	J10
hV8-2	CACAGTG	76	100	CTTGAGAATGCAAGGAGCTGAA	90	50	CACAAAGCCT	91	33	63	701		
hV8-4	CACAGTG	76	100	CTTGAGAACCTGCAAGGAGGTGAA	90	50	CATAAACCT	92	33	63	653	15830	All J area
hV8-6	CACAGTG	76	100	CCTGAGAACCTGCAAGGAGGTGAA	93	44	CACAAACCT	94	44	65	569		
hV26-2	CACAGTG	76	100	GGACAGATGGGGCTGAGCTGTG	95	56	CATAATCTC	96	33	64	345	5638	J48
hV35	CACAGTG	76	100	CTCCCCCAAAACCTGAGCCCTGT	97	94	AC1CAAACT	98	78	90	326	6520	J48
hV38-2	CACAGTG	76	100	AGACAAGGAAACGGGAGAGGCTT	99	31	ACAGAAACC	100	89	78	267	11008	J48
hV40	CACTTG	101	86	TAAAAAGGACACGTGGAGCTATA	102	44	CACAAACCT	103	44	60	233	6930	J48
hV41	CACAGTG	76	100	CTCCCCCAGGCCACCTGAGGCCGT	104	94	ACCTAAACT	105	78	90	227	5630	J48
Consensus				-T-CAG-CA-CTG-AACCTGT	106		C			%			

FIGURE 5